

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/833,245B
Source: /FW16
Date Processed by STIC: 9/12/05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 09/12/2005

PATENT APPLICATION: US/09/833,245B

TIME: 10:31:21

Input Set : N:\DA\pto.da.txt

Output Set: N:\CRF4\09122005\I833245B.raw

4 <110> APPLICANT: Human Genome Sciences, Inc.
 6 <120> TITLE OF INVENTION: Albumin Fusion Proteins
 8 <130> FILE REFERENCE: PF546
 10 <140> CURRENT APPLICATION NUMBER: 09/833,245B
 11 <141> CURRENT FILING DATE: 2001-04-12
 13 <160> NUMBER OF SEQ ID NOS: 2279
 15 <170> SOFTWARE: PatentIn Ver. 2.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 23
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Artificial Sequence
 22 <220> FEATURE:
 23 <221> NAME/KEY: primer_bind
 24 <223> OTHER INFORMATION: primer useful to clone human growth hormone cDNA
 26 <400> SEQUENCE: 1
 27 cccaagaatt cccttatcca ggc 23
 30 <210> SEQ ID NO: 2
 31 <211> LENGTH: 33
 32 <212> TYPE: DNA
 33 <213> ORGANISM: Artificial Sequence
 35 <220> FEATURE:
 36 <221> NAME/KEY: primer_bind
 37 <223> OTHER INFORMATION: primer useful to clone human growth hormone cDNA
 39 <400> SEQUENCE: 2
 40 gggaagctta gaagccacag gatccctcca cag 33
 43 <210> SEQ ID NO: 3
 44 <211> LENGTH: 16
 45 <212> TYPE: DNA
 46 <213> ORGANISM: Artificial Sequence
 48 <220> FEATURE:
 49 <221> NAME/KEY: misc_structure
 50 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
 51 with non-cohesive ends.
 53 <400> SEQUENCE: 3
 54 gataaagatt cccaac 16
 57 <210> SEQ ID NO: 4
 58 <211> LENGTH: 17
 59 <212> TYPE: DNA
 60 <213> ORGANISM: Artificial Sequence
 62 <220> FEATURE:
 63 <221> NAME/KEY: misc_structure
 64 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
 65 with non-cohesive ends.

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67 <400> SEQUENCE: 4
68 aattgttggg aatcttt 17
71 <210> SEQ ID NO: 5
72 <211> LENGTH: 17
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74 <213> ORGANISM: Artificial Sequence
76 <220> FEATURE:
77 <221> NAME/KEY: misc_structure
78 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
79 with non-cohesive ends.
81 <400> SEQUENCE: 5
82 ttaggcttat tcccaac 17
85 <210> SEQ ID NO: 6
86 <211> LENGTH: 18
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial Sequence
90 <220> FEATURE:
91 <221> NAME/KEY: misc_structure
92 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
93 with non-cohesive ends.
95 <400> SEQUENCE: 6
96 aattgttggg aataagcc 18
99 <210> SEQ ID NO: 7
100 <211> LENGTH: 24
101 <212> TYPE: PRT
102 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
105 <221> NAME/KEY: SITE
106 <222> LOCATION: 1)..(19)
107 <223> OTHER INFORMATION: invertase leader sequence
109 <220> FEATURE:
110 <221> NAME/KEY: SITE
111 <222> LOCATION: 20)..(24)
112 <223> OTHER INFORMATION: first 5 amino acids of mature human serum albumin
114 <400> SEQUENCE: 7
115 Met Leu Leu Gln Ala Phe Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys
116 1 5 10 15
118 Ile Ser Ala Asp Ala His Lys Ser
119 20
122 <210> SEQ ID NO: 8
123 <211> LENGTH: 21
124 <212> TYPE: DNA
125 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <221> NAME/KEY: misc_structure
129 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
130 fragments with non-cohesive ends.
132 <400> SEQUENCE: 8
133 gagatgcaca cctgagtgag g 21

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136 <210> SEQ ID NO: 9
137 <211> LENGTH: 27
138 <212> TYPE: DNA
139 <213> ORGANISM: Artificial Sequence
141 <220> FEATURE:
142 <221> NAME/KEY: misc_structure
143 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
144     fragments with non-cohesive ends.
146 <400> SEQUENCE: 9
147 gatcctgtgg cttcgatgca cacaaga                27
150 <210> SEQ ID NO: 10
151 <211> LENGTH: 24
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <221> NAME/KEY: misc_structure
157 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
158     fragments with non-cohesive ends.
160 <400> SEQUENCE: 10
161 ctcttggtg catcgaagcc acag                    24
164 <210> SEQ ID NO: 11
165 <211> LENGTH: 30
166 <212> TYPE: DNA
167 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
170 <221> NAME/KEY: misc_structure
171 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
172     fragments with non-cohesive ends.
174 <400> SEQUENCE: 11
175 tgtggaagag cctcagaatt tattcccaac            30
178 <210> SEQ ID NO: 12
179 <211> LENGTH: 31
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <221> NAME/KEY: misc_structure
185 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
186     fragments with non-cohesive ends.
188 <400> SEQUENCE: 12
189 aattggtggg aataaattct gaggtctcttc c          31
192 <210> SEQ ID NO: 13
193 <211> LENGTH: 47
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <221> NAME/KEY: misc_structure
199 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
200     fragments with non-cohesive ends.
202 <400> SEQUENCE: 13

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203 ttaggcttag gtggcgggtg atccggcggg ggtggatctt tcccaac 47
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207 <211> LENGTH: 48
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <221> NAME/KEY: misc_structure
213 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
214     fragments with non-cohesive ends.
216 <400> SEQUENCE: 14
217 aattgttggg aaagatccac caccgccgga tccaccgcca cctaagcc 48
220 <210> SEQ ID NO: 15
221 <211> LENGTH: 62
222 <212> TYPE: DNA
223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <221> NAME/KEY: misc_structure
227 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
228     fragments with non-cohesive ends.
230 <400> SEQUENCE: 15
231 ttaggcttag gcggtggtgg atctggtggc ggcggatctg gtggcgggtg atccttccca 60
233 ac 62
236 <210> SEQ ID NO: 16
237 <211> LENGTH: 63
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <221> NAME/KEY: misc_structure
243 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
244     fragments with non-cohesive ends.
246 <400> SEQUENCE: 16
247 aattgttggg aaggatccac cgccaccaga tccgccgcca ccagatccac caccgcctaa 60
249 gcc 63
252 <210> SEQ ID NO: 17
253 <211> LENGTH: 1782
254 <212> TYPE: DNA
255 <213> ORGANISM: Homo sapiens
257 <220> FEATURE:
258 <221> NAME/KEY: CDS
259 <222> LOCATION: (1)..(1755)
262 <400> SEQUENCE: 17
263 gat gca cac aag agt gag gtt gct cat cgg ttt aaa gat ttg gga gaa 48
264 Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
265 1 5 10 15
267 gaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag 96
268 Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
269 20 25 30
271 cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa 144
272 Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

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273		35		40		45											
275	ttt	gca	aaa	aca	tgt	gtt	gct	gat	gag	tca	gct	gaa	aat	tgt	gac	aaa	192
276	Phe	Ala	Lys	Thr	Cys	Val	Ala	Asp	Glu	Ser	Ala	Glu	Asn	Cys	Asp	Lys	
277		50					55					60					
279	tca	ctt	cat	acc	ctt	ttt	gga	gac	aaa	tta	tgc	aca	gtt	gca	act	ctt	240
280	Ser	Leu	His	Thr	Leu	Phe	Gly	Asp	Lys	Leu	Cys	Thr	Val	Ala	Thr	Leu	
281	65						70					75				80	
283	cgt	gaa	acc	tat	ggg	gaa	atg	gct	gac	tgc	tgt	gca	aaa	caa	gaa	cct	288
284	Arg	Glu	Thr	Tyr	Gly	Glu	Met	Ala	Asp	Cys	Cys	Ala	Lys	Gln	Glu	Pro	
285					85				90				95				
287	gag	aga	aat	gaa	tgc	ttc	ttg	caa	cac	aaa	gat	gac	aac	cca	aac	ctc	336
288	Glu	Arg	Asn	Glu	Cys	Phe	Leu	Gln	His	Lys	Asp	Asp	Asn	Pro	Asn	Leu	
289				100				105					110				
291	ccc	cga	ttg	gtg	aga	cca	gag	gtt	gat	gtg	atg	tgc	act	gct	ttt	cat	384
292	Pro	Arg	Leu	Val	Arg	Pro	Glu	Val	Asp	Val	Met	Cys	Thr	Ala	Phe	His	
293			115				120					125					
295	gac	aat	gaa	gag	aca	ttt	ttg	aaa	aaa	tac	tta	tat	gaa	att	gcc	aga	432
296	Asp	Asn	Glu	Glu	Thr	Phe	Leu	Lys	Lys	Tyr	Leu	Tyr	Glu	Ile	Ala	Arg	
297		130					135					140					
299	aga	cat	cct	tac	ttt	tat	gcc	ccg	gaa	ctc	ctt	ttc	ttt	gct	aaa	agg	480
300	Arg	His	Pro	Tyr	Phe	Tyr	Ala	Pro	Glu	Leu	Leu	Phe	Phe	Ala	Lys	Arg	
301	145						150				155					160	
303	tat	aaa	gct	gct	ttt	aca	gaa	tgt	tgc	caa	gct	gct	gat	aaa	gct	gcc	528
304	Tyr	Lys	Ala	Ala	Phe	Thr	Glu	Cys	Cys	Gln	Ala	Ala	Asp	Lys	Ala	Ala	
305				165				170					175				
307	tgc	ctg	ttg	cca	aag	ctc	gat	gaa	ctt	cgg	gat	gaa	ggg	aag	gct	tcg	576
308	Cys	Leu	Leu	Pro	Lys	Leu	Asp	Glu	Leu	Arg	Asp	Glu	Gly	Lys	Ala	Ser	
309				180				185					190				
311	tct	gcc	aaa	cag	aga	ctc	aaa	tgt	gcc	agt	ctc	caa	aaa	ttt	gga	gaa	624
312	Ser	Ala	Lys	Gln	Arg	Leu	Lys	Cys	Ala	Ser	Leu	Gln	Lys	Phe	Gly	Glu	
313			195				200					205					
315	aga	gct	ttc	aaa	gca	tgg	gca	gtg	gct	cgc	ctg	agc	cag	aga	ttt	ccc	672
316	Arg	Ala	Phe	Lys	Ala	Trp	Ala	Val	Ala	Arg	Leu	Ser	Gln	Arg	Phe	Pro	
317		210					215					220					
319	aaa	gct	gag	ttt	gca	gaa	gtt	tcc	aag	tta	gtg	aca	gat	ctt	acc	aaa	720
320	Lys	Ala	Glu	Phe	Ala	Glu	Val	Ser	Lys	Leu	Val	Thr	Asp	Leu	Thr	Lys	
321	225					230				235						240	
323	gtc	cac	acg	gaa	tgc	tgc	cat	gga	gat	ctg	ctt	gaa	tgt	gct	gat	gac	768
324	Val	His	Thr	Glu	Cys	Cys	His	Gly	Asp	Leu	Leu	Glu	Cys	Ala	Asp	Asp	
325				245				250					255				
327	agg	gcg	gac	ctt	gcc	aag	tat	atc	tgt	gaa	aat	cag	gat	tcg	atc	tcc	816
328	Arg	Ala	Asp	Leu	Ala	Lys	Tyr	Ile	Cys	Glu	Asn	Gln	Asp	Ser	Ile	Ser	
329			260					265					270				
331	agt	aaa	ctg	aag	gaa	tgc	tgt	gaa	aaa	cct	ctg	ttg	gaa	aaa	tcc	cac	864
332	Ser	Lys	Leu	Lys	Glu	Cys	Cys	Glu	Lys	Pro	Leu	Leu	Glu	Lys	Ser	His	
333			275				280					285					
335	tgc	att	gcc	gaa	gtg	gaa	aat	gat	gag	atg	cct	gct	gac	ttg	cct	tca	912
336	Cys	Ile	Ala	Glu	Val	Glu	Asn	Asp	Glu	Met	Pro	Ala	Asp	Leu	Pro	Ser	
337		290					295					300					

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:25; N Pos. 18,19,20,21,22,23,24,25,26,27,28,29,30,31,32
Seq#:26; N Pos. 37,38,39,40,41,42,43,44,45,46,47,48,49,50,51
Seq#:27; N Pos. 19,20,21,22,23,24,25,26,27,28,29,30,31,32,33
Seq#:28; N Pos. 38,39,40,41,42,43,44,45,46,47,48,49,50,51,52
Seq#:32; N Pos. 29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46
Seq#:33; N Pos. 38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55
Seq#:74; Xaa Pos. 24
Seq#:76; Xaa Pos. 5
Seq#:77; Xaa Pos. 29,34,37
Seq#:78; Xaa Pos. 3,17,33
Seq#:82; Xaa Pos. 196,224,233
Seq#:83; Xaa Pos. 60,73,75,82
Seq#:86; Xaa Pos. 26
Seq#:87; Xaa Pos. 50
Seq#:89; Xaa Pos. 41
Seq#:91; Xaa Pos. 13
Seq#:95; Xaa Pos. 12,38,43,145
Seq#:99; Xaa Pos. 260
Seq#:101; Xaa Pos. 259,262,280
Seq#:104; Xaa Pos. 42,49,69,76
Seq#:115; Xaa Pos. 12,49,51
Seq#:124; Xaa Pos. 7,22,24,111
Seq#:125; Xaa Pos. 81,84
Seq#:127; Xaa Pos. 1,19,81
Seq#:131; Xaa Pos. 142
Seq#:137; Xaa Pos. 42
Seq#:146; Xaa Pos. 131,185,218,220,250,312
Seq#:154; Xaa Pos. 91,93,99
Seq#:158; Xaa Pos. 36
Seq#:159; Xaa Pos. 10,19
Seq#:163; Xaa Pos. 2,6,14,34,51
Seq#:169; Xaa Pos. 6,13,51
Seq#:170; Xaa Pos. 33,129
Seq#:175; Xaa Pos. 44,57
Seq#:176; Xaa Pos. 26
Seq#:180; Xaa Pos. 71
Seq#:181; Xaa Pos. 1,5,8
Seq#:189; Xaa Pos. 21
Seq#:190; Xaa Pos. 15,30,32,187
Seq#:195; Xaa Pos. 3,17
Seq#:196; Xaa Pos. 26,28
Seq#:197; Xaa Pos. 2
Seq#:198; Xaa Pos. 27
Seq#:200; Xaa Pos. 8,12,16,18,19,23

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Output Set: N:\CRF4\09122005\I833245B.raw

Seq#:204; Xaa Pos. 9,21
Seq#:211; Xaa Pos. 79,321
Seq#:215; Xaa Pos. 8,11,18,61
Seq#:216; Xaa Pos. 8,11,18,61
Seq#:223; Xaa Pos. 36,37
Seq#:228; Xaa Pos. 98
Seq#:234; Xaa Pos. 15

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:2270; Line(s) 91695
Seq#:2271; Line(s) 91709
Seq#:2276; Line(s) 91778

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L:701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
 L:791 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
 L:880 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
 L:970 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
 L:1176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
 L:1280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
 L:1847 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74 after pos.:16
 L:1901 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:0
 L:1945 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77 after pos.:16
 M:341 Repeated in SeqNo=77
 L:1980 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78 after pos.:0
 M:341 Repeated in SeqNo=78
 L:2297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82 after pos.:192
 M:341 Repeated in SeqNo=82
 L:2349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:48
 M:341 Repeated in SeqNo=83
 L:2459 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:16
 L:2490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87 after pos.:48
 L:2550 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:89 after pos.:32
 L:2589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:91 after pos.:0
 L:2686 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95 after pos.:0
 M:341 Repeated in SeqNo=95
 L:2816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:99 after pos.:256
 L:2985 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101 after pos.:256
 M:341 Repeated in SeqNo=101
 L:3191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:104 after pos.:32
 M:341 Repeated in SeqNo=104
 L:3507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:115 after pos.:0
 M:341 Repeated in SeqNo=115
 L:3695 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:124 after pos.:0
 M:341 Repeated in SeqNo=124
 L:3752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:125 after pos.:80
 L:3894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:127 after pos.:0
 M:341 Repeated in SeqNo=127
 L:4006 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:131 after pos.:128
 L:4170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137 after pos.:32
 L:4527 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:146 after pos.:128
 M:341 Repeated in SeqNo=146
 L:4780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:154 after pos.:80
 M:341 Repeated in SeqNo=154
 L:4868 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:158 after pos.:32
 L:4901 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:159 after pos.:0
 M:341 Repeated in SeqNo=159
 L:5102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:163 after pos.:0
 M:341 Repeated in SeqNo=163
 L:5240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:169 after pos.:0
 M:341 Repeated in SeqNo=169
 L:5279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:170 after pos.:32

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M:341 Repeated in SeqNo=170

L:5410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:175 after pos.:32